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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/825,012A

DATE: 06/27/2003

TIME: 08:38:32

Input Set : A:\Sequence.txt

Output Set: N:\CRF4\06272003\I825012A.raw

3 <110> APPLICANT: Young, Robert  
5 <120> TITLE OF INVENTION: Compounds for Targeting  
7 <130> FILE REFERENCE: 43191-256808  
9 <140> CURRENT APPLICATION NUMBER: US 09/825,012A  
10 <141> CURRENT FILING DATE: 2001-04-03  
12 <150> PRIOR APPLICATION NUMBER: US 60/237,159  
13 <151> PRIOR FILING DATE: 2000-10-02  
15 <150> PRIOR APPLICATION NUMBER: GB 0008049.9  
16 <151> PRIOR FILING DATE: 2000-04-03  
18 <160> NUMBER OF SEQ ID NOS: 101  
20 <170> SOFTWARE: PatentIn version 3.1  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 282  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Homo sapiens  
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30 1 5 10 15  
33 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
34 20 25 30  
37 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
38 35 40 45  
41 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
42 50 55 60  
45 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
46 65 70 75 80  
49 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
50 85 90 95  
53 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
54 100 105 110  
57 Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
58 115 120 125  
61 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
62 130 135 140  
65 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
66 145 150 155 160  
69 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
70 165 170 175  
73 Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
74 180 185 190  
77 Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
78 195 200 205  
81 Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr

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|-----|---|-----|------|-----|
| 82  | 210   | 215 | 220  |     |
| 85  | Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly     |     |      |     |
| 86  | 225   | 230 | 235  | 240 |
| 89  | Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn     |     |      |     |
| 90  | 245   | 250 | 255  |     |
| 93  | Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser     |     |      |     |
| 94  | 260   | 265 | 270  |     |
| 97  | Asp His Tyr Pro Val Glu Val Met Leu Lys                             |     |      |     |
| 98  | 275   | 280 |      |     |
| 101 | <210> SEQ ID NO: 2  |     |      |     |
| 102 | <211> LENGTH: 1039  |     |      |     |
| 103 | <212> TYPE: DNA   |     |      |     |
| 104 | <213> ORGANISM: Homo sapiens  |     |      |     |
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| 107 | tcctgcacag gcagtgcctt gaagtgcctc ttcatcagacc tttcttcata gactactttt  |     | 60   |     |
| 109 | ttttctttaa gcagcaaaag gagaaaaattt tcatccaaagg atattccaga ttcttgacag |     | 120  |     |
| 111 | cattctcgctc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg  |     | 180  |     |
| 113 | ggggcgctgc tggcaactggc ggcctactg cagggggccg tgcctctaa gatcgccagcc   |     | 240  |     |
| 115 | ttcaacatcc agacatttgg ggagaccaag atgtccatgg ccaccctctgt cagctacatt  |     | 300  |     |
| 117 | gtgcagatcc tgagccgcta tgacatcgcc ctggccagg aggtcagaga cagccacactg   |     | 360  |     |
| 119 | actgcctgg ggaagctgct ggacaacccctt aatcaggatg caccagacac ctatcactac  |     | 420  |     |
| 121 | gtggcagtg agccactggg acggaacacgc tataaggagc gctacctgtt cgtgtacagg   |     | 480  |     |
| 123 | cctgaccagg tgcctgcggg ggacagctac tactacgtt atggctgcga gcccgcggg     |     | 540  |     |
| 125 | aacgacacct tcaaccgaga gccagccatt gtcagggtt tctcccggtt cacagaggtc    |     | 600  |     |
| 127 | agggagttt ccattgttcc cctgcatgcg gccccgggg acgcagtagc cgagatcgac     |     | 660  |     |
| 129 | gctctctatg acgtctaccc ttatgtccaa gagaatggg gcttggagga cgctatgtt     |     | 720  |     |
| 131 | atggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc    |     | 780  |     |
| 133 | ctgtggacaa gccccacctt ccagtggctg atccccgaca ggcgtacac cacagctaca    |     | 840  |     |
| 135 | cccacgcact gtgcctatga caggatcggtt gttgcaggga tgctgctccg aggcgcgtt   |     | 900  |     |
| 137 | gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg     |     | 960  |     |
| 139 | gccccagcca tcagtgcacca ctatccagtg gaggtgtgc tgaagtgc agccccc        |     | 1020 |     |
| 141 | cacaccaggta gaactgcac   |     | 1039 |     |
| 144 | <210> SEQ ID NO: 3  |     |      |     |
| 145 | <211> LENGTH: 260   |     |      |     |
| 146 | <212> TYPE: PRT   |     |      |     |
| 147 | <213> ORGANISM: Homo sapiens  |     |      |     |
| 149 | <400> SEQUENCE: 3   |     |      |     |
| 151 | Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met     |     |      |     |
| 152 | 1 5 10 15   |     |      |     |
| 155 | Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr     |     |      |     |
| 156 | 20 25 30  |     |      |     |
| 159 | Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val     |     |      |     |
| 160 | 35 40 45  |     |      |     |
| 163 | Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His     |     |      |     |
| 164 | 50 55 60  |     |      |     |
| 167 | Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr     |     |      |     |
| 168 | 65 70 75 80   |     |      |     |
| 171 | Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr     |     |      |     |
| 172 | 85 90 95  |     |      |     |

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175 Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu  
 176 100 105 110  
 179 Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe  
 180 115 120 125  
 183 Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
 184 130 135 140  
 187 Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu  
 188 145 150 155 160  
 191 Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val  
 192 165 170 175  
 195 Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe  
 196 180 185 190  
 199 Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His  
 200 195 200 205  
 203 Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala  
 204 210 215 220  
 207 Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly  
 208 225 230 235 240  
 211 Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu  
 212 245 250 255  
 215 Val Met Leu Lys  
 216 260  
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 220 <211> LENGTH: 783  
 221 <212> TYPE: DNA  
 222 <213> ORGANISM: Homo sapiens  
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 227 ctcgtcagct acatttgca gatcctgagc cgctacgaca tcgcctgtt ccaggaggtc 120  
 229 agagacagcc acctgactgc cgtggggaaag ctgtggaca acctcaatca ggacgcacca 180  
 231 gacacccatc actacgtgtt cagtggcca ctgggacgga acagctataa ggagcgctac 240  
 233 ctgttcgtgt acaggcctga ccaggtgtct gcgggtggaca gctactacta cgatgtatggc 300  
 235 tgcgagccct gcgggaaacga caccccaac cgagagccag ccattgtcag gttttctcc 360  
 237 cgggtcacag aggtcaggga gtttgcatt gttccctgc atgcggccccc gggggacgca 420  
 239 gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg 480  
 241 gaggacgtca tggatggg cgacttcaat gcgggctgca gctatgtgag accctccca 540  
 243 tggatccca tccgcctgtt gacaaggccc accttccagt ggctgatccc cgacagcgct 600  
 245 gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtggttgc agggatgctg 660  
 247 ctccgagggg cggttgttcc cgactcggtt cttccctta acttccaggc tgcctatggc 720  
 249 ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag 780  
 251 tga 783  
 254 <210> SEQ ID NO: 5  
 255 <211> LENGTH: 161  
 256 <212> TYPE: PRT  
 257 <213> ORGANISM: Homo sapiens  
 259 <400> SEQUENCE: 5  
 261 Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu  
 262 1 5 10 15  
 265 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 266 | 20  | 25  | 30  |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 269 | Phe | Gly | Glu | Thr | Lys | Met | Ser | Asn | Ala | Thr | Leu | Val | Ser | Tyr | Ile | Val |
| 270 | 35  |     |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| 273 | Gln | Ile | Leu | Ser | Arg | Tyr | Asp | Ile | Ala | Leu | Val | Gln | Glu | Val | Arg | Asp |
| 274 | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| 277 | Ser | His | Leu | Thr | Ala | Val | Gly | Lys | Leu | Leu | Asp | Asn | Leu | Asn | Gln | Asp |
| 278 | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     | 80  |     |     |     |
| 281 | Ala | Pro | Asp | Thr | Tyr | His | Tyr | Val | Val | Ser | Glu | Pro | Leu | Gly | Arg | Asn |
| 282 |     |     |     |     |     |     | 85  |     |     | 90  |     |     | 95  |     |     |     |
| 285 | Ser | Tyr | Lys | Glu | Arg | Tyr | Leu | Phe | Val | Tyr | Arg | Pro | Asp | Gln | Val | Ser |
| 286 | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |
| 289 | Ala | Val | Asp | Ser | Tyr | Tyr | Asp | Asp | Gly | Cys | Glu | Pro | Cys | Gly | Asn |     |
| 290 | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| 293 | Asp | Thr | Phe | Asn | Arg | Glu | Pro | Ala | Ile | Val | Arg | Phe | Phe | Ser | Arg | Phe |
| 294 | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| 297 | Thr | Glu | Val | Arg | Glu | Phe | Ala | Ile | Val | Pro | Leu | His | Ala | Ala | Pro | Gly |
| 298 | 145 |     |     |     |     |     | 150 |     |     |     | 155 |     | 160 |     |     |     |
| 301 | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

305 <210> SEQ ID NO: 6

306 <211> LENGTH: 858

307 <212> TYPE: DNA

308 <213> ORGANISM: Homo sapiens

310 <400> SEQUENCE: 6

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| 311 | ggcccccacca | tgagggggcat | gaagctgctg  | ggggcgctgc  | tggcactggc  | ggccctactg | 60  |
| 313 | cagggggccg  | tgtccctgaa  | gatcgacgcc  | ttcaacatcc  | agacatttgg  | ggagaccaag | 120 |
| 315 | atgtccaatg  | ccaccctcggt | cagctacatt  | gtgcagatcc  | tgagccgcta  | cgacatcgcc | 180 |
| 317 | ctgggtccagg | aggtcagaga  | cagccacctg  | actgccgtgg  | ggaagctgt   | ggacaacctc | 240 |
| 319 | aatcaggacg  | caccagacac  | ctatcactac  | gtggtcagtg  | agccactggg  | acgaaacagc | 300 |
| 321 | tataaggagc  | gctacctgtt  | cgtgtacagg  | cctgaccagg  | tgtctgcgtt  | ggacagctac | 360 |
| 323 | tactacgatg  | atggctgcga  | gccctgcggg  | aacgacacct  | tcaaccgaga  | gccagccatt | 420 |
| 325 | gtcaggttct  | tctcccggtt  | cacagagggtc | agggagtttg  | ccattgttcc  | cctgcatgcg | 480 |
| 327 | gccccggggg  | acgcagttagc | cgagatcgac  | gctctctatg  | acgtctacct  | ggatgtccaa | 540 |
| 329 | gagaaatggg  | gcttgagga   | cgtcatgtt   | atggcgcact  | tcaatgcggg  | ctgcagctat | 600 |
| 331 | gtgagaccct  | cccaagtggc  | atccatccgc  | ctgtggacaa  | gccccacctt  | ccagtggctg | 660 |
| 333 | atccccgaca  | gctgctgacac | cacagctaca  | cccacgcact  | gtgcctatga  | caggatcg   | 720 |
| 335 | gttgcaggg   | tgctgctccg  | agggggccgtt | gttcccgcact | cggctctcc   | ctttaacttc | 780 |
| 337 | caggctgcct  | atggcctgag  | tgaccaactg  | gcccaagcca  | tcagtgcacca | ctatccagtg | 840 |
| 339 | gaggtgatgc  | tgaagtga    |             |             |             |            | 858 |

342 <210> SEQ ID NO: 7

343 <211> LENGTH: 721

344 <212> TYPE: DNA

345 <213> ORGANISM: Artificial Sequence

347 <220> FEATURE:

348 <223> OTHER INFORMATION: Humanised HMFG-1 light chain

350 <400> SEQUENCE: 7

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|-----|-------------|------------|-------------|-------------|------------|------------|-----|
| 351 | atgggatgga  | gctgtatcat | cctcttcttg  | gtagcaacag  | ctacagggt  | ccactccgac | 60  |
| 353 | atccagatga  | cccagagccc | aagcagccctg | agcggccagcg | tgggtgacag | agtgaccatc | 120 |
| 355 | acctgttaagt | ccagtcagag | cctttatat   | agtagcaatc  | aaaagatcta | cttggcctgg | 180 |
| 357 | taccagcaga  | agccaggtaa | ggctccaaag  | ctgctgatct  | actgggcac  | cactaggaa  | 240 |

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| 359 | tctggtgtgc  | caagcagatt         | cagcgtagc                    | ggtagcggt  | ccgacttcac | cttcaccatc  | 300 |     |     |     |     |     |     |     |     |     |
| 361 | agcagcctcc  | agccagagga         | catcgccacc                   | tactactgcc | agcaatatta | tagatatcct  | 360 |     |     |     |     |     |     |     |     |     |
| 363 | cggacgttcg  | gccaaggggac        | caagggtggaa                  | atcaaacgaa | ctgtggctgc | accatctgtc  | 420 |     |     |     |     |     |     |     |     |     |
| 365 | ttcatcttcc  | cgcctatctga        | tgagcagttg                   | aaatctggaa | ctgcctctgt | tgtgtgcctg  | 480 |     |     |     |     |     |     |     |     |     |
| 367 | ctgaaataact | tctatcccag         | agaggccaaa                   | gtacagtgg  | aggtggataa | cgcctccaa   | 540 |     |     |     |     |     |     |     |     |     |
| 369 | tcgggtaact  | cccaggagag         | tgtcacagag                   | caggacagca | aggacagcac | ctacagcctc  | 600 |     |     |     |     |     |     |     |     |     |
| 371 | agcagcaccc  | tgacgctgag         | caaagcagac                   | tacgagaaac | acaaagtcta | cgcctgcgaa  | 660 |     |     |     |     |     |     |     |     |     |
| 373 | gtcaccatc   | agggcctgag         | ctgcggcgtc                   | acaaagagct | tcaacagggg | agagtgttag  | 720 |     |     |     |     |     |     |     |     |     |
| 375 | a           |                    |                              |            |            |             | 721 |     |     |     |     |     |     |     |     |     |
| 378 | <210>       | SEQ ID NO:         | 8                            |            |            |             |     |     |     |     |     |     |     |     |     |     |
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| 380 | <212>       | TYPE:              | DNA                          |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 381 | <213>       | ORGANISM:          | Artificial Sequence          |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 383 | <220>       | FEATURE:           |                              |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 384 | <223>       | OTHER INFORMATION: | Humanised HMFG-1 light chain |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 386 | <400>       | SEQUENCE:          | 8                            |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 387 | ggccacca    | tggatggag          | ctgtatcatc                   | ctcttcttgg | tagcaacagc | tacaggtgtc  | 60  |     |     |     |     |     |     |     |     |     |
| 389 | cactccgaca  | tccagatgac         | ccagagccca                   | agcagcctga | gcccgcgt   | gggtgacaga  | 120 |     |     |     |     |     |     |     |     |     |
| 391 | gtgaccatca  | cctgtaagtc         | oagttagcgc                   | cttttatata | gtagcaatca | aaagatctac  | 180 |     |     |     |     |     |     |     |     |     |
| 393 | ttggccttgt  | accagcagaa         | gccaggttaag                  | gctccaaagc | tgctgatcta | ctgggcattcc | 240 |     |     |     |     |     |     |     |     |     |
| 395 | actaggaaat  | ctgggtgtcc         | aaggatcc                     | agcggtagcg | gtagcggtac | cgacttcacc  | 300 |     |     |     |     |     |     |     |     |     |
| 397 | ttcaccatca  | gcagcctcca         | gccagaggac                   | atcgccaccc | actactgcca | gcaatattat  | 360 |     |     |     |     |     |     |     |     |     |
| 399 | agatatcctc  | ggacgttcgg         | ccaagggacc                   | aagggtggaa | tcaaacaac  | tgtggctgca  | 420 |     |     |     |     |     |     |     |     |     |
| 401 | ccatctgtct  | tcatcttccc         | gccatctgtat                  | gagcagttga | aatctggaa  | tgctctgtt   | 480 |     |     |     |     |     |     |     |     |     |
| 403 | gtgtgcctgc  | tgaataactt         | ctatcccaga                   | gaggccaaag | tacagtggaa | gggtggataac | 540 |     |     |     |     |     |     |     |     |     |
| 405 | gccctccaaat | cggtaactc          | ccaggagagt                   | gtcacagagc | aggacagcaa | ggacagcacc  | 600 |     |     |     |     |     |     |     |     |     |
| 407 | tacagcctca  | gcagcaccct         | gacgctgagc                   | aaagcagact | acgagaaaca | caaagtctac  | 660 |     |     |     |     |     |     |     |     |     |
| 409 | gcctgcgaag  | tcaccatca          | gggcctgagc                   | tcgcggcgtc | caaagagctt | caacaggggaa | 720 |     |     |     |     |     |     |     |     |     |
| 411 | gagtgttaga  |                    |                              |            |            |             | 730 |     |     |     |     |     |     |     |     |     |
| 414 | <210>       | SEQ ID NO:         | 9                            |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 415 | <211>       | LENGTH:            | 239                          |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 416 | <212>       | TYPE:              | PRT                          |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 417 | <213>       | ORGANISM:          | Artificial Sequence          |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 419 | <220>       | FEATURE:           |                              |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 420 | <223>       | OTHER INFORMATION: | Humanised HMFG-1 light chain |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 422 | <400>       | SEQUENCE:          | 9                            |            |            |             |     |     |     |     |     |     |     |     |     |     |
| 424 | Met         | Gly                | Trp                          | Ser        | Cys        | Ile         | Ile | Leu | Phe | Leu | Val | Ala | Thr | Ala | Thr | Gly |
| 425 | 1           |                    |                              |            |            | 5           |     |     |     | 10  |     |     |     |     | 15  |     |
| 428 | Val         | His                | Ser                          | Asp        | Ile        | Gln         | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala |
| 429 |             |                    |                              |            |            | 20          |     |     |     | 25  |     |     |     |     | 30  |     |
| 432 | Ser         | Val                | Gly                          | Asp        | Arg        | Val         | Thr | Ile | Thr | Cys | Lys | Ser | Ser | Gln | Ser | Leu |
| 433 |             |                    |                              |            |            | 35          |     |     |     | 40  |     |     |     |     | 45  |     |
| 436 | Leu         | Tyr                | Ser                          | Ser        | Asn        | Gln         | Lys | Ile | Tyr | Leu | Ala | Trp | Tyr | Gln | Gln | Lys |
| 437 |             |                    |                              |            |            | 50          |     |     |     | 55  |     |     |     |     | 60  |     |
| 440 | Pro         | Gly                | Lys                          | Ala        | Pro        | Lys         | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu |
| 441 |             |                    |                              |            |            | 65          |     |     |     | 70  |     |     |     |     | 80  |     |
| 444 | Ser         | Gly                | Val                          | Pro        | Ser        | Arg         | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe |
| 445 |             |                    |                              |            |            | 85          |     |     |     | 90  |     |     |     |     | 95  |     |
| 448 | Thr         | Phe                | Thr                          | Ile        | Ser        | Ser         | Leu | Gln | Pro | Glu | Asp | Ile | Ala | Thr | Tyr | Tyr |

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/825,012A

DATE: 06/27/2003  
TIME: 08:38:33

Input Set : A:\Sequence.txt  
Output Set: N:\CRF4\06272003\I825012A.raw

L:556 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:553  
L:1064 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:1061  
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L:7746 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:94,Line#:7743